Application No. 10/634,262
Filed: August 5, 2003
TC Art Unit: 1638
Confirmation No.: 7055

AMENDMENTS TO THE SPECIFICATION

On page 1, replace the first paragraph, beginning on line 5 with the following paragraph:

Cross-Reference to Related Application

This application is a continuation application of U.S. Patent Application No. 09/554,467 filed 12 May 2000, now U.S. Patent No. 6,639,125, which is a 371 of PCT/US98/24225 filed 12 November 1998, which is a continuation-in-part of U.S. Application No. 08/968,467 filed 12 November 1997, now U.S. Patent No. 5,981,728, all of which are incorporated by reference herein.

On page 12, replace the paragraph beginning on line 23, with the following paragraph:

Figure 6 shows the DU1 amino acid sequence is most similar to that of the potato SSIII. Figure 6A shows the primary sequence alignment. The deduced amino acid sequence of DU1 and potato SSIII (GenBank accession number X95759) are aligned. Solid directional arrows indicate that positions of the three 60 amino acid SBE-superrepeats, and dotted arrows dénote individual copies of the SBE-repeat. Dashed arrows indicate the positions of the three repeat units that make up the 85 redisue repeat. Double-headed

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arrows are labeled with Roman numerals indicate the positions of correspondingly designated conserved sequence blocks identified in the glucan synthase family (Preiss and Sivak, 1996). Figure 6B shows the domains of DU1. Similarity scores between each segment of DU1 and SSIII are shown under each region. "Catalytic domain" indicates the region of the DU1 similar in amino acid sequence to a α-(1→4)-glycosyltransferases in general. "SSIII/DU1 homology domain" indicates the region shared specifically by DU1 and SSIII among known proteins. "DU1 specific region" indicates the portion of DU1 that is unique in amino acid sequence among known proteins.

On page 21, replace the paragraph beginning at line 22 with the following paragraph:

As used herein, the term "host" is meant to include not only prokaryotes but also eukaryotes such as yeast, plant and animal cells. A recombinant DNA molecule or gene which encodes a maize starch synthase enzyme of the present invention can be used to transform a host using any of the techniques commonly known to those of ordinary skill in the art. One preferred embodiment is the use of a vectors containing coding sequences for the gene which encodes a maize starch synthase enzyme of the present invention for purposes of prokaryotic transformation. Prokaryotic

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hosts may include *E. coli*, *S. tymphimurium*, *Serratia marcescens* and *Bacillus subtilis*. Eukaryotic hosts include yeasts such as *Pichia pastoris*, mammalian cell insect cells, and more preferentially, plant cells, such as *Arabidopsis thaliana* and *Nicotiana tabacum*.

On page 47, replace the paragraph beginning at line 19 with the following paragraph:

The nature of the 180 residue repeat suggests it is involved in a specific function of DU1. The SBE-repeats that begin each SBE-superrepeat are more similar to each other than to the SBE-repeats at any of the other five portions in the superrepeat (Figure 7A). This suggests that these three SBE-repeats were not important for function, then mutations should accumulate in those sequences at the same rate that they have appeared in other portions of the SBE-superrepeat, which is not the case. The consensus sequence among these three conserved SBR-repeats is DQSIVG (SEQ ID NO. 9) in the first half-repeat, designated as the "M-box", and SHKQ (SEQ ID NO. 10) in the second half-repeat. When the M-box sequence was searched for in known polypeptides only a single type of enzyme was found to contain as exact match, namely SBEI family members.

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